DSP-5, encoded by 1020 base pairs

```
   1 GACGCGTGGC CATGTTGGAG GCTCCGGGCC CGAGTGATGG CTGCGAGCTC AGCAACCCCA
  61 GCGCCAGCAG AGTCAGCTGT GCCGGGCAGA TGCTGGAAGT GCAGCCAGGA TTGTATTTCG
 121 GTGGGGCCGC GGCCGTCGCG GAGCCAGATC ACCTGAGGGA AGCGGGCATC ACGGCCGTGC
 181 TAACAGTGGA CTCGGAGGAG CCCAGCTTCA AGGCGGGGCC TGGGGTCGAG GATCTATGGC
 241 GCCTCTTCGT GCCAGCGCTG GACAAACCCG AGACGGACCT ACTCAGCCAT CTGGACCGGT
 301 GCGTGGCCTT CATCGGTCAG GCCCGCGCTG AGGGCCGTGC GGTGTTGGTG CACTGTCATG
 361 CAGGAGTCAG TCGAAGTGTG GCCATAATAA CTGCTTTTCT CATGAAGACT GACCAACTTC
 421 CCTTTGAAAA AGCCTATGAA AAGCTCCAGA TTCTCAAACC AGAGGCTAAG ATGAATGAGG
 481 GGTTTGAGTG GCAACTGAAA TTATACCAGG CAATGGGATA CGAAGTGGAT ACCTCTAGTG
 541 CAATTTATAA GCAATATCGT TTACAAAAGG TTACAGAGAA GTATCCAGAA TTGCAGAATT
 601 TACCTCAAGA ACTCTTTGCT GTTGACCCAA CTACCGTTTC ACAAGGATTG AAAGATGAGG
 661 TTCTCTACAA GTGTAGAAAG TGCAGGCGAT CATTATTTCG AAGTTCTAGT ATTCTGGATC
 721 ACCGTGAAGG AAGTGGACCT ATAGCCTTTG CCCACAAGAG AATGACACCA TCTTCCATGC
 781 TTACCACAGG GAGGCAAGCT CAATGTACAT CTTATTTCAT TGAACCTGTA CAGTGGATGG
 841 AATCTGCTTT GTTGGGAGTG ATGGATGGAC AGCTTCTTTG CCCAAAATGC AGTGCCAAGT
 901 TGGGTTCCTT CAACTGGTAT GGTGAACAGT GCTCTTGTGG TAGGTGGATA ACACCTGCTT
 961 TTCAAATACA TAAGAATAGA GTGGATGAAA TGAAAATATT GCCTGTTTTG GGATCACAAA
1021 CAGGAAAAAT ATGAACATGA TATTTTATAG CTTGGGAAGA AACTTGCAGA TGATATGTGC
1081 TGCCTTTGCT TCTTATCATT CATGGC
```

Fig. 1

Alternate form of DSP-5, encoded by 897 base pairs

```
  1 GACGCGTGGC CATGTTGGAG GCTCCGGGCC CGAGTGATGG CTGCGAGCTC AGCAACCCCA
 61 GCGCCAGCAG AGTCAGCTGT GCCGGGCAGA TGCTGGAAGT GCAGCCAGGA TTGTATTTCG
121 GTGGGGCCGC GGCCGTCGCG GAGCCAGATC ACCTGAGGGA AGCGGGCATC ACGGCCGTGC
181 TAACAGTGGA CTCGGAGGAG CCCAGCTTCA AGGCGGGGCC TGGGGTCGAG GATCTATGGC
241 GCCTCTTCGT GCCAGCGCTG GACAAACCCG AGACGGACCT ACTCAGCCAT CTGGACCGGT
301 GCGTGGCCTT CATCGGTCAG GCCCGCGCTG AGGGCCGTGC GGTGTTGGTG CACTGTCATG
361 CAGGAGTCAG TCGAAGTGTG GCCATAATAA CTGCTTTTCT CATGAAGACT GACCAACTTC
421 CCTTTGAAAA AGCCTATGAA AAGCTCCAGA TTCTCAAACC AGAGGCTAAG ATGAATGAGG
481 GGTTTGAGTG GCAACTGAAA TTATACCAGG CAATGGGATA CGAAGTGGAT ACCTCTAGTG
541 CAATTTATAA GCAATATCGT TTACAAAAGG TTACAGAGAA GTATCCAGAA TTGCAGAATT
601 TACCTCAAGA ACTCTTTGCT GTTGACCCAA CTACCGTTTC ACAAGGATTG AAAGATGAGG
661 TTCTCTACAA GTGTAGAAAG TGCAGGCGAT CATTATTTCG AAGTTCTAGT ATTCTGGATC
721 ACCGTGAAGG AAGTGGACCT ATAGCCTTTG CCCACAAGAG AATGACACCA TCTTCCATGC
781 TTACCACAGG GAGGCAAGCT CAATGTACAT CTTATTTCAT TGAACCTGTA CAGTGGATGG
841 AATCTGCTTT GTTGGGAGTG ATGGATGGAC AGGTGAGAAC ACATTTTATT TTCTACAATT
901 TTATTTTATG ATCTATATTT TATTCCTTCT TGCATTTTAA GCTCTATTTT AACTAGTGTT
961 TTGCTCCATT TCTTAATTTC TTTATTTCTG ATGATTATAT CTTTCTTGTG TAGATAA
```

Fig. 2

DSP-5, predicted peptide sequence of 340 amino acids

MLEAPGPSDGCELSNPSASRVSCAGQMLEVQPGLYFGGAAAVAEPDHLREAGITAVLTVDSEEPSFKAGP
GVEDLWRLFVPALDKPETDLLSHLDRCVAFIGQARAEGRAVLVHCHAGVSRSVAIITAFLMKTDQLPFEK
AYEKLQILKPEAKMNEGFEWQLKLYQAMGYEVDTSSAIYKQYRLQKVTEKYPELQNLPQELFAVDPTTVS
QGLKDEVLYKCRKCRRSLFRSSSILDHREGSGPIAFAHKRMTPSSMLTTGRQAQCTSYFIEPVQWMESAL
LGVMDGQLLCPKCSAKLGSFNWYGEQCSCGRWITPAFQIHKNRVDEMKILPVLGSQTGKI*

Fig. 3

Alternate form of DSP-5, predicted peptide sequence of 299 amino acids

MLEAPGPSDGCELSNPSASRVSCAGQMLEVQPGLYFGGAAAVAEPDHLREAGITAVLTVDSEEPSFKAGP
GVEDLWRLFVPALDKPETDLLSHLDRCVAFIGQARAEGRAVLVHCHAGVSRSVAIITAFLMKTDQLPFEK
AYEKLQILKPEAKMNEGFEWQLKLYQAMGYEVDTSSAIYKQYRLQKVTEKYPELQNLPQELFAVDPTTVS
QGLKDEVLYKCRKCRRSLFRSSSILDHREGSGPIAFAHKRMTPSSMLTTGRQAQCTSYFIEPVQWMESAL
LGVMDGQVRTHFIFYNFIL*

Fig. 4

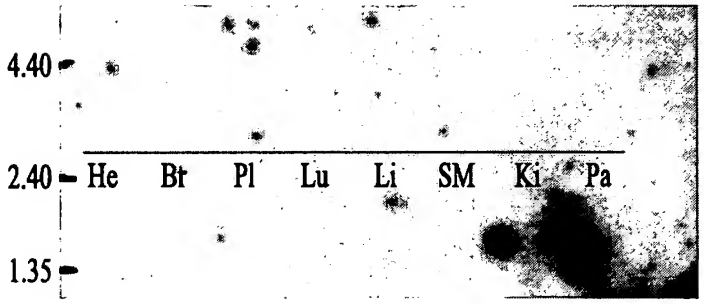
```
                1        10        20        30        40        50        60        70        80        90       100
                |--------+---------+---------+---------+---------+---------+---------+---------+---------+--------|
PYST1,          SDLDRD-PNSATDSDGSPLSNSQPSFPV-EILPFLYLGCAKDSTNLDVLEEFGIKYILNVTPNLPNLFENAG--EFKYKQIPISDHWSQNLSQFFPEAIS
MKP-7,             DRELPSSATESDGSPVPSSQPAFPV-QILPYLYLGCAKDSTNLDVLGKYGIKYILNVTPNLPNAFEHGG--EFTYKQIPISDHWSQNLSQFFPEAIS
hVH5            GLCEGKPAALLPMSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASNSCPKP-DFIC--ESRFMRVPINDNYCEKLLPWLDKSIE
PAC1            PAQALPPAGAENSNSDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAVLNVSASCPNHFE--G--LFHYKSIPVEDNQMVEISAWFQEAIS
MKP-1,          PLSTSVPDSAESGCSSCSTPLYDQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSANCPNHFE--G--HYQYKSIPVEDNHKADISSWFNEAID
MKP-4,          PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSSDCPNHFE--G--HYQYKCIPVEDNHKADISSWFMEAIE
MKP-5,          SERALISQCGKPYYNVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSRRTSEACM--T--HLHYKWIPVEDSHTADISSHFQEAID
DSP-5           MLEAPGPSDGCELSNPSASRVSCAGQMLEYQPGLYFGGAAAYAEPDHLREAGITAVLTVDSEEPSFKAGPGVEDLWRLFVPALDKPETDLLSHLDRCVA
Consensus         l a  p                  gg  e!lP LYlGsa      # $   gItavLnvs   p      g     yk !P  D    dlss f ea!

                101     110       120       130       140       150       160       170   176
                |-------+---------+---------+---------+---------+---------+---------+-----|
PYST1,          FIDEARGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTLGLSS
MKP-7,          FIDEARSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLSS
hVH5            FIDKAKLSSCQVIVHCLAGISRSATIAIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLLA
PAC1            FIDSVKNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH
MKP-1,          FIDSIKNRGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPH
MKP-4,          YIDAVKDCRGRVLVHCQAGISRSATICLAYLMMKKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLATS
MKP-5,          FIDCVREKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMVSPNFGFMGQLLQYESEILPSTPN
DSP-5           FIGQARAEGRSVLVHCHAGVSRSVAIITAFLMKTDQLPFEKAYEKLQILKPEAKMNEGFEWQLKLYQAMGYEVDT
Consensus       FId ar  g  VlVHC AG!SRS t!  A%lnkt       A% fvk rr  ispNf FngQLl y#
```

Fig. 5

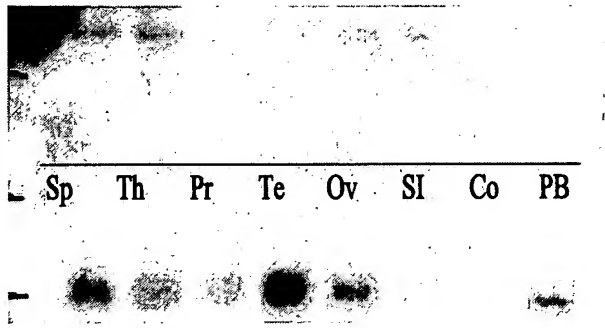
DSP-5

- Northern blot analysis



- He = Heart
- Br = Brain
- Pl = Placenta
- Lu = Lung
- Li = Liver
- SM = Skel. Muscle
- Ki = Kidney
- Pa = Pancreas

Fig. 6A



- Sp = Spleen
- Th = Thymus
- Pr = Prostate
- Te = Testis
- Ov = Ovaries
- SI = Small Intestine
- Co = Colon
- PB = Priph. Blood

Fig. 6B